

REPLACEMENT SHEET

Fig. 15A

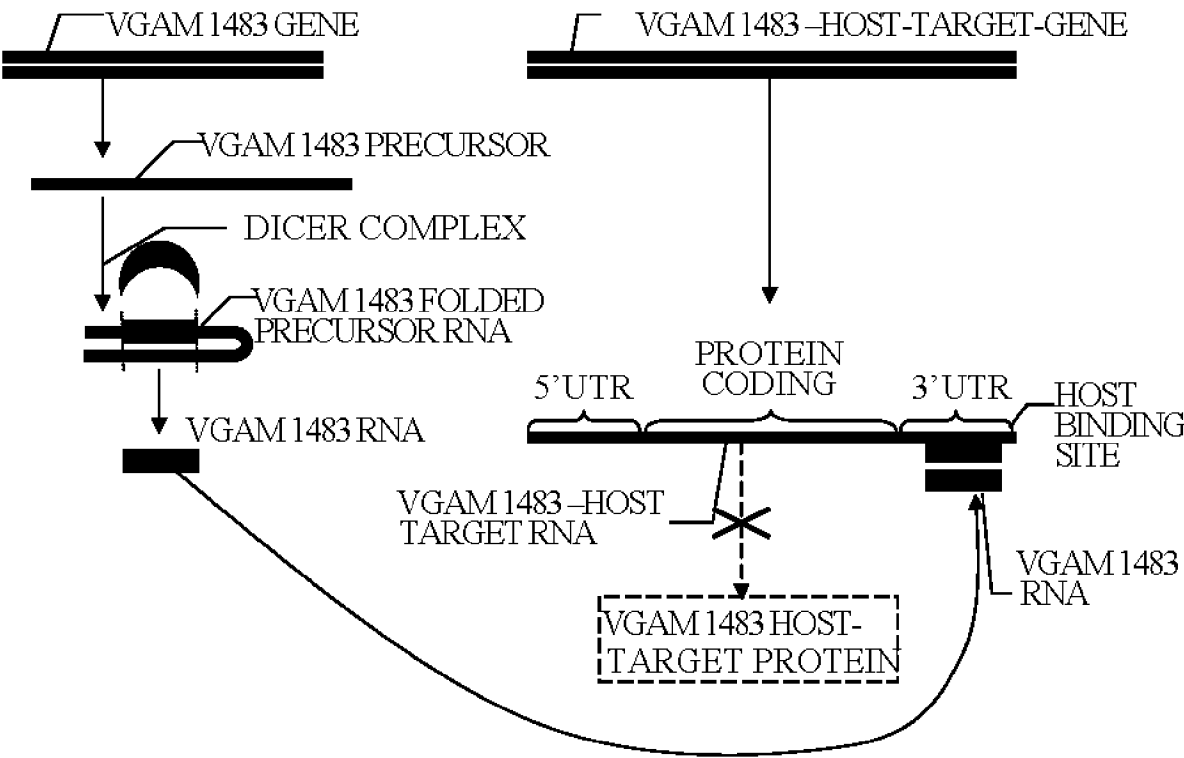


Fig. 15B

GTGTGACGTGAGTCTGATCCAACACTGAACGCTTTCGTC SEQ ID: 37404  
GTGTTTTTCATGCAGCTTTTACAGACCATGACAAGCCTGA  
CGAGAGCGTTCATCGGGGCATGAAGTACGCATTACAC

TGACAAGCCTGACGAGAGCGTTCA SEQ ID: 37405

Fig. 15C

--	AG	-	A	AACAC		T	T	CAG	TT	
GTGTGA	CGTG	TC	TG	TCC		TGAACGCTTTCGTCG	GTTT	TCATG	CT	T
CACATT	GCAT	AG	AC	GGG		<u>ACTTGCGAGAGCAGT</u>	<u>CGAA</u>	<u>AGTAC</u>	GA	/
AC	GA	T	-	GCT--		<u>C</u>	<u>C</u>	CA-	CA	

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**Fig. 15D/1**

<b>C7 BINDING SITE</b>	5' TGA CAA GCCTGA CGA GAGCGTTCA 3'	SEQ ID:37405
	3' ACT CGGACT CTCGTAAGT 5'	SEQ ID:37406
	ATC TAC	
<b>DUSP5 BINDING SITE</b>	5' TG A CAAGCCTG ACGA G GA CGTTCA 3'	SEQ ID:37405
	3' AC GTTCGGAC CT GTGAGT 5'	SEQ ID:37407
	- CA-- G	
<b>ATP6V1F BINDING SITE</b>	5' TG A CAAGCCTG AC GAGAG 3'	SEQ ID:37405
	3' AC GTTCGGAC CTCTC 5'	SEQ ID:37408
	C CC	
<b>DKFZP564C103 BINDING SITE</b>	5' TGA CAA GCCTGACG AGAGCG TTCA 3'	SEQ ID:37405
	3' ACT CGGACTGC AAGT 5'	SEQ ID:37409
	AC- GAGAG-	
<b>KIAA0561 BINDING SITE</b>	5' GA CA C TGACGAGAG GT 3'	SEQ ID:37405
	3' CT TCG ACTGCTCTC CA 5'	SEQ ID:37410
	AC A C	
<b>KIAA0935 BINDING SITE</b>	5' TG A CAAGCCTG A G A C AG GC 3'	SEQ ID:37405
	3' AC GTTCGGAC G TC CG 5'	SEQ ID:37411
	C C - C	
<b>MIC2L1 BINDING SITE</b>	5' GACAAGCCTGACGAG AGC GTTCA 3'	SEQ ID:37405
	3' CTGTTTCGGACTGTTT CAAGT 5'	SEQ ID:37412
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<b>PPP4R1L BINDING SITE</b>	5' TGACAAG CTGA C C- GAGAGCG 3'	SEQ ID:37405
	3' ACTGTTT GACT TTCTCGC 5'	SEQ ID:37413
	A AC	
<b>ZAK BINDING SITE</b>	5' TGACAAGCC TGACG GC- AGA GTTC 3'	SEQ ID:37405
	3' ACTGTTCGG TCT CAAG 5'	SEQ ID:37414
	----- AGT	

# REPLACEMENT SHEET

**Fig. 15D/2**

		CC ACGA		
	5'	TGACAAG TG	GAGCGTT	3'
LOC149566				
BINDING SITE	3'	ACTGTTC AC	CTTGCAA	5'
		A- CCA-		
				SEQ ID:37405
				SEQ ID:37415
		A AC G CG		
	5'	TG CAAGCCTG	GA AG TTC	3'
LOC150368				
BINDING SITE	3'	AC GTTCGGAC	CT TC GAG	5'
		C A- G A-		
				SEQ ID:37405
				SEQ ID:37416
		A CGAGA C		
	5'	TGACA GCCTGA	G GTTC	3'
LOC255718				
BINDING SITE	3'	ACTGT CGGACT	C CAGG	5'
		C ----- C		
				SEQ ID:37405
				SEQ ID:37417